

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: November 6, 2004, 19:24:00 ; Search time 66.875 Seconds
(without alignments)
43.019 Million cell updates/sec

Title: US-10-618-644-1
Perfect score: 26
Sequence: 1 YVVPK 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	46	Q72Y55	Q72Y55 bacillus ce
2	26	100.0	46	Q81XH0	Q81XH0 bacillus an
3	26	100.0	46	AAS44067	AAS44067 bacillus
4	26	100.0	46	AAT34399	AAT34399 bacillus
5	26	100.0	83	R31B TROW8	Q83hg6 tropheryma
6	26	100.0	83	R31B TROWT	Q83gh5 tropheryma
7	26	100.0	92	Q854U4	Q854U4 mycobacteri
8	26	100.0	127	Q9DJ44	Q9DJ44 spodoptera
9	26	100.0	137	Q0FI SCHPO	P78929 schizosacch
10	26	100.0	142	Q8H7B7	Q8H7B7 arabidopsis
11	26	100.0	146	1ADF6 ARATH	Q9zsk2 arabidopsis
12	26	100.0	146	Q8LCM6	Q8LCM6 arabidopsis
13	26	100.0	153	Q8ERR4	Q8err4 oceanobacil
14	26	100.0	159	1SRP COXBU	Q81c29 coxiella bu
15	26	100.0	165	Q8W2Y3	Q8w2y3 oryza sativ
16	26	100.0	165	Q65145	Q65145 african swi
17	26	100.0	191	Q7M211	Q7m211 glycine soj
18	26	100.0	228	Q8ZUL3	Q8zul3 pyrobaculum
19	26	100.0	233	Q6WS55	Q6ws55 staphylococ
20	26	100.0	233	AAQ75791	AAQ75791 staphyloc
21	26	100.0	238	Q7M210	Q7m210 glycine soj
22	26	100.0	240	Q39858	Q39858 glycine max
23	26	100.0	242	Q8TYF1	Q8tyf1 methanopyru
24	26	100.0	247	1CDH ENTCL	Q9z6c1 enterobacte
25	26	100.0	249	Q8K101	Q8kl01 rhizobium e
26	26	100.0	250	Q6BXS1	Q6bxs1 debaryomyce
27	26	100.0	251	1CDH SALTU	P62219 salmonella
28	26	100.0	259	Q6MQF2	Q6mqf2 bdellovibri
29	26	100.0	259	CAE78495	CAE78495 bdellovib
30	26	100.0	262	Q8R6H7	Q8r6h7 thermoanaer
31	26	100.0	308	Q43671	Q43671 vicia faba

32 26 100.0 312 2 017998 017998 caenorhabdi
33 26 100.0 312 2 CAB04643 Cab04643 caenorhab
34 26 100.0 317 2 Q9ZVR6 Q9zvr6 arabidopsis
35 26 100.0 328 2 Q53709 Q53709 staphylococ
36 26 100.0 331 2 Q9FHB5 Q9fhb5 arabidopsis
37 26 100.0 336 2 Q6NPT8 Q6npt8 arabidopsis
38 26 100.0 336 2 AAR20786 Aar20786 arabidops
39 26 100.0 338 1 LEGB_PEA P14594 pisum sativ
40 26 100.0 343 2 Q8L588 Q8l588 brassica na
41 26 100.0 346 2 Q8TVQ7 Q8tvq7 methanopyru
42 26 100.0 346 2 Q38886 Q38886 arabidopsis
43 26 100.0 346 2 Q9SQH3 Q9sqh3 brassica na
44 26 100.0 346 2 Q9FJ47 Q9fj47 arabidopsis
45 26 100.0 349 2 Q6FP45 Q6fp45 candida gla

ALIGNMENTS

RESULT 1

Q72Y55 PRELIMINARY; PRT; 46 AA.
AC Q72Y55;
DT 05-JUL-2004 (TRMBLrel. 27, Created)
DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BCES166;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
ON NCBI_TaxID=22523;
RX [1]
RX SEQUENCE FROM N.A.
RX PubMed=14960714;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pX01.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017280; AAS44067.1; -.
DR TIGR; BCE5166; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 46 AA; 5103 MW; 77601C6E92B48CBD CRC64;

Query Match 100.0%; Score 26; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVVPK 5
| | | | |
Db 14 YVVPK 18

RESULT 2

Q81XH0 PRELIMINARY; PRT; 46 AA.
AC Q81XH0; Q6KKM0;
DT 01-JUN-2003 (TRMBLrel. 24, Created)
DT 01-JUN-2003 (TRMBLrel. 24, Last sequence update)
DT 01-OCT-2004 (TRMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BA5267; ORFNames=GBAA5267;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
ON NCBI_TaxID=1392;
RX [1]
RX SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate Porton;
RC MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Oekstad O.A., Helgason E., Riststone J., Wu M.,

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RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RA "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative Genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017040; AAP28932.1; -.
DR ENBL; AE017334; AAT34399.1; -.
DR TIGR; BA5267; -.
KW Hypothetical protein.
SQ SEQUENCE 46 AA; 5055 MW; F5601C6E92B49410 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVWFK 5
DB 14 YVWFK 18

RESULT 3
ID AAS44067 PRELIMINARY; PRT; 46 AA.
AC AAS44067;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 04-MAY-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN BCE5166.
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Routs D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RA "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017280; AAS44067.1; -.
DR TIGR; BCE5166; -.
KW Hypothetical protein.
SQ SEQUENCE 46 AA; 5103 MW; 77601C6E92B48CBD CRC64;

Query Match 100.0%; Score 26; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVWFK 5
DB 14 YVWFK 18

RESULT 4
AAT34399 PRELIMINARY; PRT; 46 AA.
ID AAT34399
AC AAT34399;

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DT 01-JUN-2004 (T-EMBLrel. 27, Created)
DT 01-JUN-2004 (T-EMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN GBAA5267.
OS Bacillus anthracis str. Ames 0581.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group; Bacillus anthracis.
OX NCBI_TaxID=261594;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S., Fraser C.M.;
RT "Bacillus anthracis comparative Genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017334; AAT34399.1; -.
KW Hypothetical protein.
SQ SEQUENCE 46 AA; 5055 MW; F5601C6E92B49410 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVWFK 5
DB 14 YVWFK 18

RESULT 5
R31B TROWS
ID R31B TROWS STANDARD; PRT; 83 AA.
AC Q83RQ6;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 50S ribosomal protein L31 type B.
GN Name=rpME2; Synonyms=rpME; OrderedLocusNames=TW458;
OS Tropheryma whippieii (strain TW08/27) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcaceae; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=218496;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22495039; PubMed=12606174;
RA Bentley S.D., Maitwald M., Murphy L.D., Pallen M.J., Yeats C.A.,
RA Dover L.G., Norbertczak H.T., Besra G.S., Quail M.A., Harris D.E.,
RA von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
RA Barrell B.G., Parkhill J., Rellman D.A.;
RT "Sequencing and analysis of the genome of the Whipple's disease
RL bacterium Tropheryma whippieii.";
RL Lancet 361:637-644(2003).
CC -!- SIMILARITY: Belongs to the L31P family of ribosomal proteins.
CC Subfamily B.
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CC -----
DR EMBL; BX251411; CAD67126.1; -.
DR HAMAP; MF_00502; -.
DR InterPro; IPR002150; Ribosomal_L31.
DR Pfam; PF01197; Ribosomal_L31; 1.
DR PRINTS; PR01249; RIBOSOMAL_L31.
DR TIGRFAMs; TIGR00105; L31; 1.
DR PROSITE; PS01143; RIBOSOMAL_L31; 1.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 83 AA; 9807 MW; C8AFF09B7F818313 CRC64;

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Query Match 100.0%; Score 26; DB 1; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVVEK 5
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Db 11 YVVEK 15

RESULT 6
R31B_TROWT STANDARD; PRT; 83 AA.
ID R31B_TROWT
AC Q854U4 PRELIMINARY; PRT; 92 AA.
DT 23-MAR-2004 (Rel. 43, Created)
DT 23-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 50S ribosomal protein L31 type B.
GN Names: rplM2; Synonyms: rplM2; OrderedLocusNames: TWT314;
OS Tropheryma whipplei (strain Twist) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcales; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=203267;
RN [1]
SEQUENCE FROM N.A.

RP MEDLINE=22784088; PubMed=12902375; DOI=10.1101/gr.1474603;
RA Raoult D., Ogata H., Audic S., Robert C., Suhr K., Drancourt M.,
Claverie J.-M.;
RT "Tropheryma whipplei Twist: a human pathogenic Actinobacteria with a
reduced genome."
RL Genome Res. 13:1800-1809(2003).
CC -1- SIMILARITY: Belongs to the L31P family of ribosomal proteins.
CC Subfamily B.

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DR EMBL; AE016851; AAC44411.1; -;
DR HAMAP; MF 00502; -; 1.
DR InterPro; IPR002150; Ribosomal_L31.
DR Pfam; PF01197; Ribosomal_L31; 1.
DR PRINTS; PR01249; RIBOSOMALL31.
DR TIGRFAMs; TIGR00105; L31; 1.
DR PROSITE; PS01143; RIBOSOMAL_L31; 1.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 83 AA; 9807 MW; C8AFF09B7F818313 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVVEK 5
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|
|
Db 11 YVVEK 15

RESULT 7
Q854U4 PRELIMINARY; PRT; 92 AA.
ID Q854U4
AC Q854U4
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp56.
OS Mycobacteriophage Che9C.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=205872;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=22592660; PubMed=12705866;
RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Panunzio N.R.,
Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
Hatfull G.F.;
RT "Origins of highly mosaic mycobacteriophage genomes."
RL Cell 113:171-182(2003).
DR EMBL; AV129333; AAN12614.1; -;
SQ SEQUENCE 92 AA; 10239 MW; 2903022ED34CBA37 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVVEK 5
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Db 49 YVVEK 53

RESULT 8
Q9DJ44 PRELIMINARY; PRT; 127 AA.
ID Q9DJ44
AC Q9DJ44;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Spodoptera litura multicapsid nucleopolyhedrovirus (SpitMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=46242;
RN [1]
RP SEQUENCE FROM N.A.
RA Li Z., Long Q., Wei Y., Zheng J., Pang Y., Wang X.;
RT "Sequence Analysis of the Alkaline Exonuclease Gene of Spodoptera
RT litura Nucleopolyhedrovirus."
RL Zhongshan Da Xue Xue Bao Zi Ran Ke Xue Ban 39:0-0(2000).
RN [2]
RP SEQUENCE FROM N.A.

RX STRAIN=G2;
RC MEDLINE=21425398; PubMed=11531416;
RA Pang Y., Yu J., Wang L., Hu X., Bao W., Li G., Chen C., Han H., Hu S.,
Yang H.;
RT "Sequence analysis of the Spodoptera litura multicapsid
RT nucleopolyhedrovirus genome."
RL Virology 287:391-404(2001).
DR EMBL; AY008144; AAG22850.1; -;
DR EMBL; AF325155; AAL01794.1; -;
DR InterPro; IPR011029; DEATH_like.
KW Hypothetical protein.
SQ SEQUENCE 127 AA; 14818 MW; 88B94214B84C9A63 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVVEK 5
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|
Db 78 YVVEK 82

RESULT 9
COFI_SCHPO STANDARD; PRT; 137 AA.
ID COFI_SCHPO
AC P78929;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cofilin.
GN Names: cofil; ORFNames=SPAC20G4.06c;
OS Schizosaccharomyces pombe (Fission yeast).
OX Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jägers K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quayl M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shipakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomycetes pombe";
 RL Nature 415:871-880(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Kawamukai M.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Controls reversibly actin polymerization and
 CC depolymerization in a pH-sensitive manner. It has the ability to
 CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
 CC major component of intranuclear and cytoplasmic actin rods (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
 CC -----
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 CC -----
 DR EMBL; D89939; BAAL4039.1; -;
 DR EMBL; Z98600; CAB11258.1; -;
 DR PIR; T43245; T43245.
 DR HSPSP; Q03048; 1COF.
 DR GeneDB SPombe; SPAC2024.06c; -;
 DR InterPro; IPR002108; Actbind_cofln.
 DR Pfam; PF00241; Cofilin_ADF; 1.
 DR PRINTS; PR00006; COFILIN.
 DR ProDom; PD002129; Actbind_cofln; 1.
 DR SMART; SM00102; ADF; 1.
 DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
 DR ACTIN-binding; Cytoskeleton.
 FT DOMAIN 88 107
 SQ SEQUENCE 137 AA; 15620 MW; ECC6D3354C959E04 CRC64;
 Query Match 100.0%; Score 26; DB 1; Length 137;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis

QY 1 YVWFK 5
 DB 27 YVWFK 31
 RESULT 10
 Q8H7B7 PRELIMINARY; PRT; 142 AA.
 AC Q8H7B7;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stracke R., Palme K.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF083753; AANG0311.1; -;
 DR InterPro; IPR001623; DnaJ_N.
 DR PROSITE; PS00636; DnaJ_1; UNKNOWN 1.
 KW Hypothetical protein.
 FT NON_TER 142 142
 SQ SEQUENCE 142 AA; 16373 MW; EF072F53947D6104 CRC64;
 Query Match 100.0%; Score 26; DB 2; Length 142;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YVWFK 5
 DB 59 YVWFK 63
 RESULT 11
 ADF6_ARATH STANDARD; PRT; 146 AA.
 ID ADF6_ARATH
 AC Q9ZSK2; Q93VZ4; Q9SUX6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Actin-depolymerizing factor 6 (ADF-6) (AtADF6).
 GN Name=ADF6; OrderedLocusNames=At2g31200; ORFNames=F16D14.4;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21307188; PubMed=11414611; DOI=10.1023/A:1010687911374;
 RA Dong C.-H., Kost B., Xia G., Chua N.-H.;
 RT "Molecular identification and characterization of the Arabidopsis
 RT ADF6, ADF5 and ADF4 genes";
 RL Plant Mol. Biol. 45:517-527(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell K.S., Ketchum K.A., Lee J.J., Renning C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis

thaliana.";
RL Nature 402:761-768(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Aneari Y.,
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Khan S., Kosema E., Tshida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
genome.";
RL Science 302:842-846(2003).
CC -!- FUNCTION: Actin-depolymerizing protein. Severs actin filaments (P-
CC actin) and binds to actin monomers.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: Belongs to the actin-binding proteins ADF family.
CC -----
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CC -----
DR EMBL; AF102824; AAD09112.1; -
DR EMBL; AF183576; AAF01035.1; -
DR EMBL; AC006593; AAD20665.2; -
DR EMBL; AY057119; AAL15349.1; -
DR EMBL; AF372880; AAK49596.1; ALT_INIT.
DR HSSP; Q39250; 1F7S.
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD00129; Actbind_cofin; 1.
DR SMART; SM00102; ADF; 1.
DR SQU SEQUENCE 146 AA; 16708 MW; A97CF5D2CC17A85 CRC64;
Query Match 100.0%; Score 26; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YVWFK 5
DB 36 YVWFK 40
RESULT 12
Q8LCLM6 PRELIMINARY; PRT; 146 AA.
ID Q8LCLM6
AC Q8LCLM6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Actin-depolymerizing factor ADF-6.
OS Arabidopsis thaliana (mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=22088475; PubMed=12093376;
RA Haas B.J., Volfovsky N., Town C.D., Troupkan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troupkan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY086510; AAM63510.1; -
DR HSSP; Q39250; 1F7S.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD00129; Actbind_cofin; 1.
DR SMART; SM00102; ADF; 1.
DR SQU SEQUENCE 146 AA; 16722 MW; A97CE99EBD4EA185 CRC64;
Query Match 100.0%; Score 26; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YVWFK 5
DB 36 YVWFK 40
RESULT 13
Q8ERR4 PRELIMINARY; PRT; 153 AA.
ID Q8ERR4
AC Q8ERR4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcriptional regulator (Arac/Xylis family).
GN OrderedLocustNames=OB1237;
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831;
RX MEDLINE=22220767; PubMed=12235376;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; AF004597; BAC13193.1; -
DR InterPro; IPR010499; Arac_E_bind.
DR InterPro; IPR011256; Bac_Reg_effector.
DR Pfam; PF06445; Arac_E_bind; 1.
DR Complete proteome.
DR SQU SEQUENCE 153 AA; 17844 MW; 5997641FE7DC0374 CRC64;
Query Match 100.0%; Score 26; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YVWFK 5
DB 91 YVWFK 95
RESULT 14
SSRP COXBU STANDARD; PRT; 159 AA.
ID -SSRP COXBU
AC Q83C29;

DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE SsrA-binding protein.
GN Name=smpB; OrderedLocusNames=CBU1305;
OS Coccidia burnetii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Coccidiaceae; Coccidia.
OX NCBI_TaxID=777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nine Mile Phase I / RSA 493;
RX MEDLINE=22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;
RA Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
RA Nelson W.C., Ward N.L., Tettelin H., Daviden T.M., Beanan M.J.,
RA DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
RA Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
RA Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
RT "Complete genome sequence of the Q-fever pathogen, Coccidia
burnetii.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
CC -!- FUNCTION: Binds specifically to the ssrA RNA (tmRNA) and is
CC required for stable association of ssrA with ribosomes (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the smpB family.
CC -----
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CC -----
DR EMBL; AEO16964; AAO90811.1; -;
DR HSSP; O66640; 1P6V.
DR TIGR; CBU1305; -;
DR HAMAP; MF_00023; -; 1.
DR InterPro; IPR000037; SmpB.
DR Pfam; PF01668; SmpB; 1.
DR ProDom; PD004488; SmpB; 1.
DR TIGRFAMs; TIGR000086; smpB; 1.
DR PROSITE; PS01317; SSRP; 1.
KW Complete proteome; RNA-binding.
SQ SEQUENCE 159 AA; 18456 MW; 084C0A1CA2409F25 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVWFK 5
Db 55 YVWFK 59
|||||
RESULT 15
ID Q8W2Y3 PRELIMINARY; PRT; 165 AA.
AC Q8W2Y3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein OSUNB0060105.7 (Hypothetical protein
DE OSJNBa0053C23.31).
DE OSJNBa0053C23.31.
GN ORFNames=OSJNBa0053C23.31, OSJNBb0060105.7;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.

RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pal G.,
RA Vanaken S.E., Uterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.L., Beta J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
RA Uterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
RT chromosome 10.";
RL Science 300:1566-1569(2003).
RN [6]
RP SEQUENCE FROM N.A.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC092697; AAL58116.1; -;
DR EMBL; AC092389; AAM8636.1; -;
DR EMBL; AE017115; AAP34802.1; -;
DR Gramene; Q8W2Y3; -;
KW Hypothetical protein.
SQ SEQUENCE 165 AA; 19567 MW; D2D8A457DAC46C79 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVWFK 5
Db 136 YVWFK 140
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Search completed: November 6, 2004, 19:52:47
Job time : 74.875 secs